AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

Claims 1-4 (canceled).

Claim 5 (currently amended): A method for detecting a mutation which causes or is associated with long QT syndrome comprising amplifying any one of ~~exons 1-15 of~~ exons 1-6 and 8-15 of HERG with a pair of primers such that the entire exon, and no other exon or portion thereof, is amplified, and analyzing the amplified exon for a mutation which causes or is associated with long QT syndrome.

Claim 6 (currently amended): The method of claim 5, wherein the pair of primers is selected from the group consisting of:

a) SEQ ID NOs:56 and 57;

b) SEQ ID NOs:58 and 59;

c) SEQ ID NOs:60 and 61;

d) SEQ ID NOs:62 and 63;

e) SEQ ID NOs:64 and 65;

f) SEQ ID NOs:66 and 67;

g) SEQ ID NOs:68 and 69;

h) SEQ ID NOs:70 and 71;

~~i) SEQ ID NOs:76 and 77;~~

j)SEQ ID NOs:78 and 79;

k) SEQ ID NOs:80 and 81;

l) SEQ ID NOs:82 and 83;

m) SEQ ID NOs:84 and 85;

n) SEQ ID NOs:86 and 87;

o) SEQ ID NOs:88 and 89;

p) SEQ ID NOs:90 and 91;

q) SEQ ID NOs:92 and 93; and

r) SEQ ID NOs:94 and 95.

Claim 7 (previously presented): The method of claim 5, wherein the analyzing step is performed by singe-stranded conformation polymorphism technique.

Claim 8 (previously presented): The method of claim 6, wherein the analyzing step is performed by singe-stranded conformation polymorphism technique.

Claim 9 (previously presented): The method of claim 5, wherein the analyzing step is performed by sequencing the amplified exon.

Claim 10 (previously presented): The method of claim 6, wherein the analyzing step is performed by sequencing the amplified exon.

Claim 11 (new): A method for detecting a mutation which causes or is associated with long QT syndrome comprising amplifying any two or more of exons 1-15 of HERG with a pair of primers for each exon such that the entire exon, and no other exon or portion thereof, is amplified for each of the two or more exons, and analyzing the amplified exons for a mutation which causes or is associated with long QT syndrome.

Claim 12 (new): The method of claim 11, wherein the pairs of primers is selected from the group consisting of:

a) SEQ ID NOs:56 and 57;

b) SEQ ID NOs:58 and 59;

c) SEQ ID NOs:60 and 61;

d) SEQ ID NOs:62 and 63;

e) SEQ ID NOs:64 and 65;

f) SEQ ID NOs:66 and 67;

g) SEQ ID NOs:68 and 69;

h) SEQ ID NOs:70 and 71;

i) SEQ ID NOs:76 and 77;

j) SEQ ID NOs:78 and 79;

k) SEQ ID NOs:80 and 81;

l) SEQ ID NOs:82 and 83;

m) SEQ ID NOs:84 and 85;

n) SEQ ID NOs:86 and 87;

o) SEQ ID NOs:88 and 89;

p) SEQ ID NOs:90 and 91;

q) SEQ ID NOs:92 and 93; and

r) SEQ ID NOs:94 and 95.

Claim 13 (new): The method of claim 11, wherein the analyzing step is performed by singe-stranded conformation polymorphism technique.

Claim 14 (new): The method of claim 12 wherein the analyzing step is performed by singe-stranded conformation polymorphism technique.

Claim 15 (new): The method of claim 11, wherein the analyzing step is performed by sequencing the amplified exon.

Claim 16 (new): The method of claim 12, wherein the analyzing step is performed by sequencing the amplified exon.

Claim 17 (new): The method of claim 11, wherein all 15 exons of HERG are amplified.